SEQUENCE LISTING

(1) GENERAL INFORMATION

   (I) APPLICANTS:
        Lenting, Hermanus Bernardus Maria
        Van Beckhoven, Rudolf Franciscus Wilhelmus Cornelis
        Maurer, Karl-Heinz
        Kottwitz, Beatrix
        Weiss, Albrecht
        Van Solingen, Pieter

   (ii) TITLE OF INVENTION:
        Detergents Comprising Cellulases

   (iii) NUMBER OF SEQUENCES:
        Two

   (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Henkel Corporation
        (B) STREET: 140 Germantown Pike, Suite 150
        (C) CITY: Plymouth Meeting
        (D) STATE: Pennsylvania
        (E) COUNTRY: U.S.A.
        (F) ZIP: 19462

   (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: 3.5" diskette
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: MS-DOS
        (D) SOFTWARE: MS Word 6.0

   (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
             U.S. Ser. No. 08/945,574
        (B) FILING DATE:
             unavailable
        (C) CLASSIFICATION: (IPC)
             C12N 9/42
             C11D 3/386

   (vii) PRIOR APPLICATION DATA
        (A) APPLICATION NUMBERS:
             PCT/EP96/01755
             EP 95201115.3
             U.S. 614,115
        (B) FILING DATES:
             26 Apr. 1996
             28 Apr. 1995
             12 Mar. 1996

(viii)ATTORNEY/AGENT INFORMATION:
    (A) NAME: Murphy, Glenn E. J.
    (B) REGISTRATION NUMBER: 33,539
    (C) REFERENCE/DOCKET NUMBER: H 1920 PCT/US

(ix)TELECOMMUNICATION INFORMATION:
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    (C) E-MAIL: Glenn.Murphy @ Henkel-Americas.com

B3

27

(2)   INFORMATION FOR SEQ ID NO: 1

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 467 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (C) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

Met Lys Lys Ile Thr Thr Ile Phe Ala Val Leu Leu Met Thr Leu Ala
-26 -25   -20   -15

Leu Phe Ser Ile Gly Asn Thr Thr Ala Ala Asp Asp Tyr Ser Val Val
-10   -5   1   5

Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu Val Asn Glu
              10   15   20

Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His Gly Leu Gln
          25   30   35

Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp Leu Arg Asp
    40   45   50

Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr Ser Ser Gly
55   60   65   70

Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys Glu Thr Val
              75   80   85

Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp Trp His Ile
              90   95   100

Leu Ser Asp Asn Asp Pro Asn Ile Tyr Lys Glu Glu Ala Lys Asp Phe
        105   110   115

Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn Val Ile Tyr
    120   125   130

Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp Asp Asn Gln
135   140   145   150

Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg Asp Asn Asp
          155   160   165

Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser Gln Asp Val
          170   175   180

His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val Met Tyr Ala
        185   190   195

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Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg Asp Gln Val
    200             205         210

Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser Glu Trp Gly
215             220             225             230

Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp Glu Ala Gln
            235             240             245

Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp Ala Asn Trp
            250             255             260

Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met Pro Gly Ala
            265             270             275

Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro Ser Gly Thr
    280             285             290

Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Ile Pro Pro Ser Asp
295             300             305             310

Pro Thr Pro Pro Ser Asp Pro Gly Glu Pro Asp Pro Gly Glu Pro Asp
            315             320             325

Pro Thr Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn
            330             335             340

Gln Ile Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln
    345             350             355

Ala Lys Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro
    360             365             370

Trp Glu Pro Leu Lys Ser Asp Pro Asp Ser Gly Glu Pro Asp Pro Thr
375             380             385             390

Pro Pro Ser Asp Pro Gly Glu Tyr Pro Ala Trp Asp Ser Asn Gln Ile
            395             400             405

Tyr Thr Asn Glu Ile Val Tyr His Asn Gly Gln Leu Trp Gln Ala Lys
            410             415             420

Trp Trp Thr Gln Asn Gln Glu Pro Gly Asp Pro Tyr Gly Pro Trp Glu
        425             430             435

Pro Leu Asn
    440
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(3)   INFORMATION FOR SEQ ID NO: 2

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 574 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

Met Lys Trp Met Lys Ser Met Val Trp Leu Ala Val Val Leu Val Val
 1   5   10   15

Ser Phe Val Ala Pro Ala Val Ser Ser Ala Asn Glu Asp Val Lys Thr
            20   25   30

Leu Asp Ile Gln Ser Tyr Val Arg Asp Met Gln Pro Gly Trp Asn Leu
        35   40   45

Gly Asn Thr Phe Asp Ala Val Gly Gln Asp Glu Thr Ala Trp Gly Asn
    50   55   60

Pro Arg Val Thr Arg Glu Leu Ile Glu Arg Ile Ala Asp Glu Gly Tyr
65   70   75   80

Lys Ser Ile Arg Ile Pro Val Thr Trp Glu Asn Arg Ile Gly Gly Ala
            85   90   95

Pro Asp Tyr Pro Ile Asp Pro Gln Phe Leu Asn Arg Val Asp Glu Val
            100   105   110

Val Gln Trp Ala Leu Glu Glu Asp Leu Tyr Val Met Ile Asn Leu His
        115   120   125

His Asp Ser Trp Leu Trp Ile Tyr Glu Met Glu His Asn Tyr Asn Gly
    130   135   140

Val Met Ala Lys Tyr Arg Ser Leu Trp Glu Gln Leu Ser Asn His Phe
145   150   155   160

Lys Asp Tyr Pro Thr Lys Leu Met Phe Glu Ser Val Asn Glu Pro Lys
            165   170   175

Phe Ser Gln Asn Trp Gly Glu Ile Arg Glu Asn His His Ala Leu Leu
            180   185   190

Asp Asp Leu Asn Thr Val Phe Phe Glu Ile Val Arg Gln Ser Gly Gly
        195   200   205

Gln Asn Asp Ile Arg Pro Leu Val Leu Pro Thr Met Glu Thr Ala Thr
    210   215   220

B3

30

Ser Gln Pro Leu Leu Asn Asn Leu Tyr Gln Thr Ile Asp Lys Leu Asp
225   230   235   240

Asp Pro Asn Leu Ile Ala Thr Val His Tyr Tyr Gly Phe Trp Pro Phe
                245   250   255

Ser Val Asn Ile Ala Gly Tyr Thr Arg Phe Glu Glu Asp Ser Lys Arg
                260   265   270

Glu Ile Ile Glu Thr Phe Asp Arg Val His His Thr Phe Val Ala Arg
        275   280   285

Gly Ile Pro Val Val Leu Gly Glu Phe Gly Leu Leu Gly Phe Asp Lys
        290   295   300

His Thr Gly Val Ile Gln Gln Gly Glu Lys Leu Lys Phe Phe Glu Tyr
305   310   315   320

Leu Ile His His Leu Asn Glu Arg Asp Ile Thr His Met Leu Trp Asp
                325   330   335

Asn Gly Gln His Phe Asn Arg His Thr Tyr Glu Trp Tyr Asp Glu Glu
                340   345   350

Leu Phe Asp Met Leu Arg Ala Ser Trp Gly Gly Arg Ser Ser Val Ala
        355   360   365

Glu Ser Asn Phe Ile Tyr Leu Lys Gln Gly Asp Arg Ile Ala Asp Ala
    370   375   380

Thr Val Thr Leu Gln Leu His Gly Asn Glu Leu Thr Gly Leu Gln Ala
385   390   395   400

Asn Gly Gln Arg Leu Thr Pro Gly Gln Asp Tyr Glu Leu Asn Gly Glu
                405   410   415

Arg Leu Thr Val Lys Ala His Val Leu Ser Ala Ile Ala Gly Ser Gly
                420   425   430

Thr Leu Gly Thr Asn Gly Met Val Thr Ala Glu Phe Asn Arg Gly Ala
        435   440   445

Asp Trp His Phe Arg Val Asn Thr Tyr Arg Thr Pro Val Leu Gln Ser
    450   455   460

Thr Gln Gly His Val Ser Asn Phe Ser Ile Pro Ala Ser Phe Asn Gly
465   470   475   480

Asn Ser Leu Ala Thr Met Glu Ala Val Tyr Val Asp Gly Gly Asn Ala
                485   490   495

Gly Pro Gln Asp Trp Thr Ser Phe Lys Glu Phe Gly Tyr Ala Phe Ser
                500   505   510

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Pro Ser Tyr Asp Thr His Glu Ile Lys Leu Thr Glu Ala Phe Phe Arg
        515                 520              525

Glu Val Arg Asp Gly Glu Val Arg Leu Thr Phe His Phe Trp Ser Gly
        530                 535              540

Glu Ile Val Asn Tyr Thr Ile Ile Lys Asn Gly Asn Gln Val Thr Gly
545                 550              555                  560

Ile Ala Ala Gln Thr Thr Asn Ser Lys Asn Lys Asn Lys Lys
            565              570
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